

[illegible]

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G S L A L W S D A P T L D P S A A N T S G L P G V P W A A A	38
TTTG GCT GGG GCA TTG CTG CGG CTG GCC ACG GTG GGA GGC AAC CTG CTG GTA ATC ATA GCC ATC GCC CGC ACG CCG AGA CTA CAG ACC ATA	771
L A G A L L A L A L A T V G G N L L V I I A I A R T P R L Q T I	68
ACC AAC GTG TTC GTG ACT TCA CTG GCC GCA GCT GAC TTG GTA GTG GGA CTC CTG GTA ATG CCA CCA GGG GCC ACA TTG GCG CTG ACT GGC	861
T N V F V T S L A A A D L V V G L L V M P P G A T L A L T G	98
CAT TGG CCC TTG GGC GAA ACT GGT TGC GAA CTG TGG ACG TCA GTG GAC GTG CTC TGT GTA ACT GCT AGC ATC GAG ACC TTG TGC GCC CTG	951
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GCT GTG GAC CGC TAC CTA GCT ACC CCT TTG CGT TAC GGC ACG GTT ACC AAG CGC CGC GGC GCG GCA GTT GTC CTG GTG	1041
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N P V I Y C R S P D F R D A F R R L L C S Y G G R G P E P	368
CGC GCA GTC ACC TTC CCA GCC AGC CCT GTT GAA GCC AGG CAG AGT CCA CCG CTC AAC AG	1771
R A V T F P A S P V E A R Q S P L N R Donor 1	387

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FIG. 3

AMINO-ACID SEQUENCE OF THE HUMAN B3-ADRENERGIC RECEPTOR GENE

10	20	30	40	50	60	70	80
MAPWPHENSS	LAPWDLPTL	APNTANTSGL	PGVPWEAALA	GALLALAVLA	TVGGNLLVIV	AIAWTPRLQT	MTNVFVTSLA
90	100	110	120	130	140	150	160
AADLVMGLLV	VPPAATLALT	GHWPLGATGC	ELWTSVDVLC	VTASIELTCA	LAVDRYLAVT	NPLRYGALVT	KRCARTAVVL
170	180	190	200	210	220	230	240
VWVVSAAVSF	APIMSQWWRV	GADAEAQRCH	SNPRCCAFAS	NMPYVLLSSS	VSFYLPLLVM	LFVYARVFVV	ATRQLRLLRG
250	260	270	280	290	300	310	320
ELGRFPPEES	PPAPSRSLAP	APVGTCAPPE	GVPACGRRPA	RLPLPREHRA	LCTLGLIMGT	FTLCWLPFFL	ANVLRALGGP
330	340	350	360	370	380	390	400
SLVPGPAFLA	LNWLGYSANSA	FNPLIYCRSP	DFRSAFRRL	CRCGRRLPPE	PCAAARPALF	PSGVPAARSS	PAQPRLCQRL

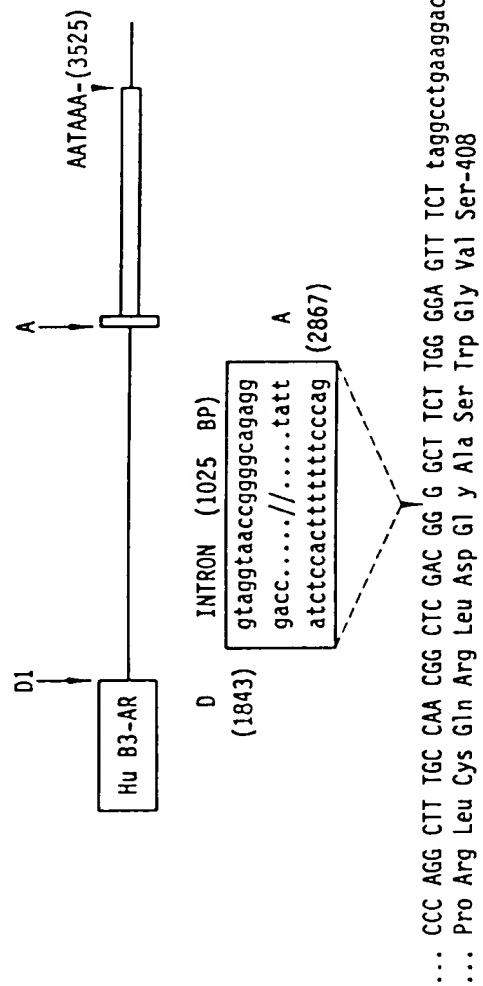
DGASWGV

FIG. 4

AMINO-ACID SEQUENCE OF THE MOUSE B3-ADRENERGIC RECEPTOR GENE

10	20	30	40	50	60	70	80
MAPWPHRNGS	LALWSDAPTL	DPSAANTSGL	PGVPWAAALA	GALLALATVG	GNLLVIIAIA	RTPRLQITN	VFVTSLAAAD
90	100	110	120	130	140	150	160
LVVGLLMPP	GATLALTGHW	PLGETGCELW	TSVDVLCVTA	SIETLCALAV	DRYLAVTNPL	RYGTLVTKRR	ARAAVVLVWI
170	180	190	200	210	220	230	240
VSAAVSFAP	MSQWVRVGAD	AEAECHSNP	RCCSFASNMP	YALLSSSVSF	YLPLLVMLFV	YARVFVAKR	QRHLLRREL
250	260	270	280	290	300	310	320
RFSPEESPPS	PSRSPSPATG	GTPAAPDGV	PCGRPARLL	PLREHRLRT	LGLIMGIFSL	CWLPFFLANV	LRALAGPSLV
330	340	350	360	370	380	390	400
PSGVFIALNW	LGYSANSAFNP	VIYCRSPDFR	DAFRRLCSY	GGRGPEEPRA	VTFPASPVEA	RQSPPLNRFD	GYEGARPFPT

FIG. 5A



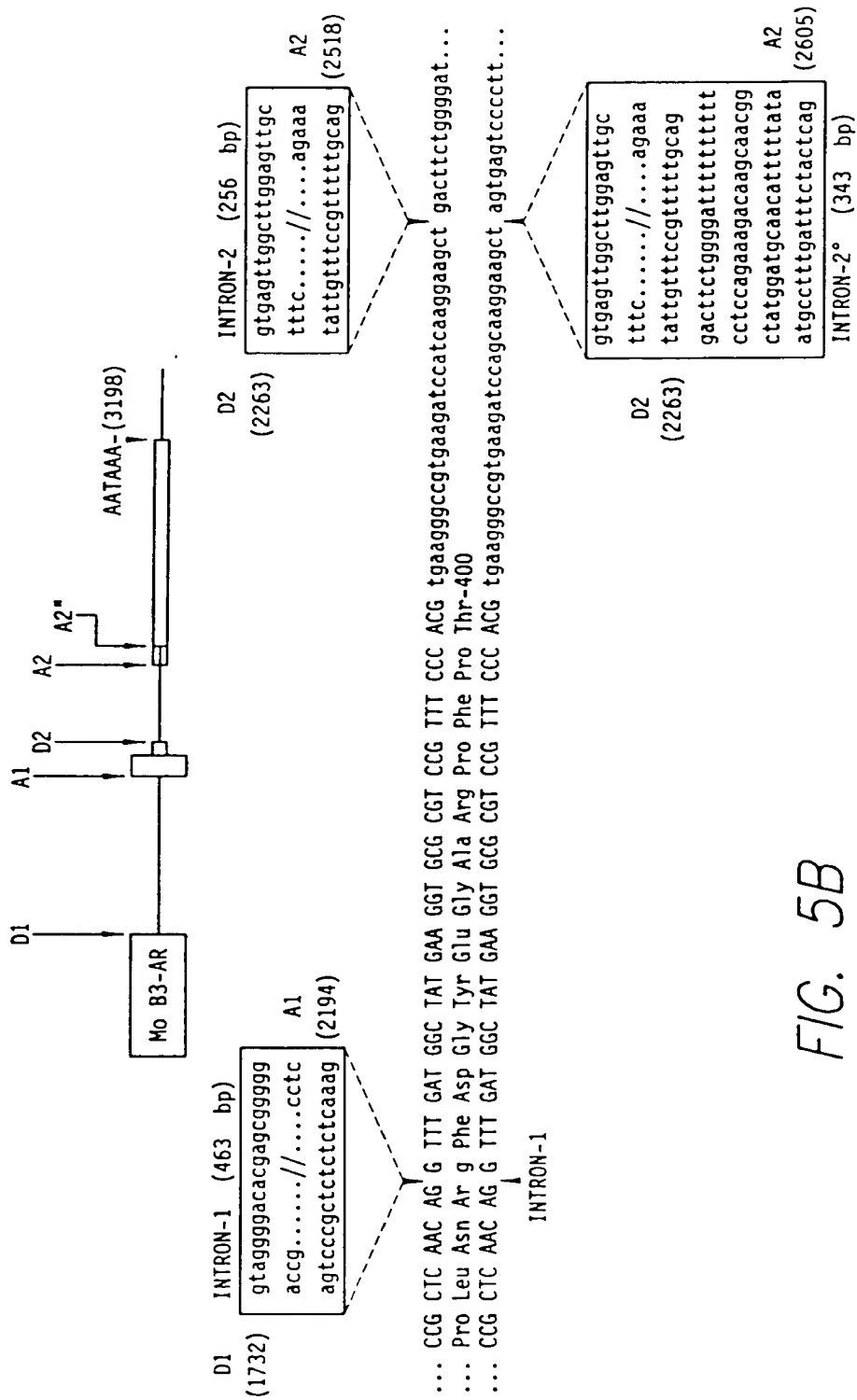


FIG. 5B